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Research Article

Taxonomic and phylogenetic analyses reveal two new *Comoclathris* taxa (Dothideomycetes, Pleosporaceae) from Inner Mongolia, China

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Abstract

The Inner Mongolia Autonomous Region, located in northern China, represents a temperate semi-arid ecosystem dominated by steppe vegetation and characterized by rich, yet understudied, fungal diversity. During an investigation of microfungi associated with decaying plant materials in the desert regions of Inner Mongolia, two novel species of *Comoclathris* were collected and isolated. Detailed morphological examinations and multi-locus phylogenetic analyses based on ITS, LSU, SSU, and *rpb*2 sequence data support the establishment of these taxa as novel species: *Comoclathris desertica* and *C. xiangshawanensis*. These two species are described and illustrated herein, with particular attention to their differences from similar species with respect to ascomatal structures and ascospore morphology. The discovery of these new taxa expands the known diversity and distribution of *Comoclathris* in China and provides new insights into the saprobic fungal communities of semi-arid regions. This study also highlights the ecological and taxonomic significance of continued surveys on saprobic fungi in grassland and desert ecosystems of northern China.

Key words: 2 new species, desert, Dothideomycetes, Pleosporales, saprobes

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Introduction

Comoclathris Clem. is a genus of ascomycetous fungi belonging to Pleosporaceae Nitschke (Pleosporales, Dothideomycetes). The genus was established by Clements (1909), with *C. lanata* Clem. designated as the type species. Previously, the genus *Comoclathris* was placed in Diademaceae Shoemaker & C.E. Babc. (Shoemaker and Babcock 1992), but recent morphological

and molecular phylogenetic analyses have supported its placement in Pleosporaceae (Zhang et al. 2012; Ariyawansa et al. 2015; Hyde et al. 2024). Currently, 52 epithets of *Comoclathris* are listed in Index Fungorum (2026), with molecular data available for only 21 species in NCBI. This genus is characterized by ascomata with circular lid-like openings, cylindrical to clavate asci, and muriform ascospores that are reddish-brown to dark brown and applanate (Mattoo et al. 2023). While most *Comoclathris* species are mainly saprobic on woody substrates, dead stems, and leaves of various plants or soil (Wanasinghe et al. 2015; Thambugala et al. 2017; Brahmanage et al. 2020; Crous et al. 2021), some are endophytes (González-Menéndez et al. 2018; Mattoo et al. 2023) and phytopathogens (Moral et al. 2017). *Comoclathris* is a widely distributed genus, found in many countries and regions, as detailed in recent publications (Mattoo et al. 2023; Xu et al. 2024). *Comoclathris* was first reported in China by Xu et al. (2024), who described two novel species from Jilin and Yunnan provinces.

The Inner Mongolia Autonomous Region is located in northern China and lies within a temperate semi-arid zone, with ecological types covering typical steppe, meadow steppe, desert steppe, as well as sandy land and forest-steppe transition zones (Han et al. 2009; Su et al. 2011; Yan et al. 2025). The vegetation of this region is dominated by herbaceous plants of the Asteraceae Bercht. & J.Presl, Fabaceae Lindl., and Poaceae (R. Brown) Barnhart families, and although steppe vegetation predominates, the types are relatively diverse rather than strictly monotypic (Fu et al. 2021; Wang et al. 2024). Despite this lack of vegetation diversity, fungi are important in these regions, as they may harbour new species with significant bioprospecting potential. Recent studies have shown that the fungal communities in Inner Mongolia exhibit considerable diversity. For example, analyses from 63 root samples during a study of ectomycorrhizal (EM) fungi revealed 288 operational taxonomic units (OTUs) spanning 31 lineages, indicating that fungal communities in forest/forest-edge environments may be much more diverse than anticipated (Wang et al. 2021). Further studies on arbuscular mycorrhizal (AM) fungi in grassland environments conducted by Wang et al. (2020) revealed 24 species spanning across eight genera. Despite increasing research on fungal diversity in Inner Mongolia Autonomous Region, detailed data and systematic taxonomic studies on saprobic fungi remain scarce. To date, only a few saprobic fungal novelties have been reported from Inner Mongolia, for example, *Diatrype betulaceicola* Z.E. Yang and Hai X. Ma, with polysporous asci described by Yang et al. (2022). The unique ecological conditions of the semi-arid grassland ecosystem in this region make saprobic fungi crucial in decomposing plant debris, cycling nutrients, and maintaining soil fertility. Therefore, studying the taxonomy of saprobic fungi is essential to unravel their hidden fungal diversity and potential applications.

Our ongoing studies in this region explore the diversity of saprobic ascomycetes inhabiting dead plant material in the desert regions of Inner Mongolia, specifically the Xiangshawan Scenic Area. During a survey of microfungi from decaying substrates, two species of *Comoclathris* were collected and examined. Morphological characteristics and phylogenetic analyses based on multi-locus sequence data (ITS, LSU, SSU, and *rpb*2) were employed to confirm their taxonomic placement within Pleosporaceae and support their establishment as novel species. This study provides new insights into the saprobic fungal diversity of northern China and expands the known distribution and species richness of the genus *Comoclathris*.

Materials and methods

Sample collection, morphological observation, single-spore isolation and preservation

During a fungal resource survey in the desert areas of Inner Mongolia Autonomous Region, China (Fig. 1), dead fallen branches and stems with fungal fruiting bodies were collected. Important information was recorded during the collection process (collector, date, location, and habitat) (Rathnayaka et al. 2024). After that, the samples were placed in dry plastic bags for further observation and experimentation in the laboratory. Morphological structures were examined by using an OPTEC SZ650 dissecting stereomicroscope (Chongqing, China), and the microstructures of fungi were observed and photographed by using an OLYMPUS optical microscope (Tokyo, Japan) with an OLYMPUS DP74 (Tokyo, Japan) digital camera. Micro-morphological structures were measured in the Tarosoft ® Image Framework program v. 1.3. The photo plates were edited in Adobe Photoshop CS3 Extended version 22.0.0 software (Adobe Systems, California, USA).

Fungi were isolated and cultured using the single-spore isolation method described by Senanayake et al. (2020). The experiment was conducted under a sterile environment. After the work surface was disinfected with 75% alcohol, an alcohol lamp was lit. First, fresh fruiting bodies were observed and selected, then cut open with a sterile blade. Spores were picked up with a sterile needle, placed in sterile water and dispersed, and finally transferred to potato dextrose agar (PDA) plates (100 mL/plate) using a pipette. From 6 hours after inoculation to 48 hours, spores were checked promptly after germination with a sterile needle and then placed on a new PDA plate at 23–28 °C. Four germinated spores were transferred to each plate. After colonies formed, the morphology was observed to ensure consistency and confirm the results of the single-spore isolation experiment. The colonies were purified and used for molecular experiments, observed for sporulation, and photographed.

Figure 1. Vegetation and habitat in the desert area of Xiangshawan Scenic Area.

Specimens were deposited at Guizhou Medical University (GMB-W), China. Living cultures are deposited in the Guizhou Medical University Culture Collection (GMBCC), China. Facesoffungi (FoF) numbers were assigned as described by Jayasiri et al. (2015), and MycoBank (MB) numbers were assigned as outlined at https://www.mycobank.org/.

DNA extraction, PCR amplification, and sequencing

Total genomic DNA was extracted from one-month-old fresh fungal mycelium (grown on PDA). The DNA Extraction Kit-BSC14S1 (BioFlux, Hangzhou, P.R. China) was used following the manufacturer's instructions. Polymerase chain reactions (PCR) were carried out using the following primers: The internal transcribed spacer (ITS) region was amplified with the primers ITS4 and ITS5 (White et al. 1990), 28S nrRNA gene (LSU) was amplified by using the primers LR0R and LR5 (Vilgalys and Hester 1990), 18S ribosomal RNA (SSU) was amplified using the primers NS1 and NS4 (White et al. 1990), and the partial RNA polymerase II subunit (*rpb*2) region was amplified with primers fRPB2-5F and fRPB2-7cR (Liu et al. 1999). The PCR thermal cycle programs for ITS, LSU, and SSU were as follows: an initialization step of 94 °C for 3 min, followed by 35 cycles of 94 °C for 30 s, an annealing step at 55 °C for 50 s, an elongation step at 72 °C for 1 min and a final extension step of 72 °C for 10 min; and the PCR thermal cycle programs for *rpb*2 was as follows: an initialization step of 95 °C for 3 min, followed by 40 cycles of 95 °C for 50 s, an annealing step at 57 °C for 50 s, an elongation step at 72 °C for 90 s and a final extension step of 72 °C for 10 min (Du et al. 2025). The DNA amplification procedure was performed by PCR in a 25 µL reaction containing 12.5 µL 2xMaster Mix (mixture of Easy Taq TM DNA Polymerase, dNTPs, and optimized buffer (Beijing Trans Gen Biotech Co., Chaoyang District, Beijing, China)), 8.5 µL ddH_2O, 2 µL of DNA template, and 1 µL of each forward and reverse primer (10 pM). Purification and sequencing of PCR products were carried out by Sangon Biotech Co., Kunming, China.

Phylogenetic analyses

A combined dataset of ITS, LSU, SSU, and *rpb*2 was used for the phylogenetic analyses. The quality of the raw sequences was checked in BioEdit v.7.2.6.1 (Hall 1999), and the forward and reverse sequences were spliced with Geneious 9.1.8 (Kearse et al. 2012). Sequences obtained from this study were searched in the GenBank database (http://blast.ncbi.nlm.nih.gov/) using BLAST to identify the closely related taxa of our strains. The additional sequences included in the analyses were collected from previous publications (Mattoo et al. 2023; Xu et al. 2024) and downloaded from GenBank (Benson et al. 2013). Phylogenetic analyses were carried out with 41 sequences (Table 1). The FASTA file was used for constructing the Randomized Accelerated Maximum Likelihood (RAxML) and Bayesian Inference analyses (BI) was performed using the OFPT (Zeng et al. 2023) with the protocol. Then, the FASTA file was converted to PHYLIP and NEXUS formats in ALTER for RAxML and BI phylogenetic analyses, respectively (Glez-Peña et al. 2010).

The CIPRES Science Gateway platform was used to carry out the RAxML and BI analyses (Miller et al. 2010). The RAxML tree, generated with 1,000 bootstrap replicates, was analyzed using RAxML-HPC2 on XSEDE (8.2.12) (Stamatakis et al. 2008; Stamatakis 2014) with the GTR+I+G model of evolution and bootstrap support. The BI tree was performed with MrBayes on XSEDE (3.2.7a) (Ronquist et al. 2012) by the Markov Chain Monte Carlo (MCMC) method to evaluate posterior probabilities (BYPP) (Richard and Lippmann 1991; Rannala and Yang 1996; Zhaxybayeva and Gogarten 2002). The best-fit nucleotide substitution models for each dataset were then selected using the Bayesian information criterion (BIC) from 22 common DNA substitution models with rate heterogeneity, as implemented in ModelFinder (Kalyaanamoorthy et al. 2017). The best model for ITS was TIM2e+I+G4, K2P+I for LSU, TPM2u+F+I for SSU, and TN+F+G4 for *rpb*2. Six simultaneous Markov chains were run for 2,000,000 generations, and a tree was sampled every 100th generation. The phylogenetic tree was visualized in FigTree v.1.4.2 (Rambaut 2012) and edited in Microsoft PowerPoint 2021 and Adobe Photoshop CS3 Extended version 22.0.0 (Adobe Systems, California, USA). All newly generated sequences in this study were deposited in GenBank (https://www.ncbi.nlm.nih.gov/WebSub/?form=history&tool=genbank).

Table 1. Taxa names, strain numbers, and corresponding GenBank accession numbers of the taxa included in the present study. Remarks: The newly generated sequences are indicated in bold, the superscript ^{T} indicates ex-type, and "—" indicates information unavailable.

Taxon name	Strain number	ITS	LSU	SSU	*rpb*2	References
Comoclathris acuminata	MCC9771^{T}	MW205771	OQ547244	—	—	Mattoo et al. (2023)
C. acuminata	MN3-2019	OQ547243	OQ547245	—	—	Mattoo et al. (2023)
C. ambigua	CBS 366.52	KY940748	AY787937	—	KT216533	Woudenberg et al. (2017)
C. antarctica	WA0000074564^{T}	MW040594	MW040597	—	—	Crous et al. (2021)
C. arrhenatheri	MFLUCC 15-0465^{T}	KX965737	KY000647	KX986348	KX938346	Thambugala et al. (2017)
C. arrhenatheri	MFLUCC 15-0476	KY026595	KY000648	KX986349	—	Thambugala et al. (2017)
C. clematidis	CCMJ 13076^{T}	OQ534243	OQ534239	OQ676454	OQ547800	Xu et al. (2024)
C. clematidis	CCMJ 13077	OQ534244	OQ534240	OQ676455	OQ547801	Xu et al. (2024)
C. compressa	CBS 156.53	—	KC584372	KC584630	KC584497	Woudenberg et al. (2013)
C. compressa	CBS 157.53	—	MH868679	KC584631	KC584498	Woudenberg et al. (2013)
C. desertica	**GMBCC2307^{T}**	**PX660512**	**PX660516**	**PX660508**	**PX672979**	**This study**
C. desertica	**GMBCC2320**	**PX660513**	**PX660517**	**PX660509**	**PX672980**	**This study**
C. europaeae	MFLU 20-0391^{T}	MT370396	MT370421	MT370367	MT729650	Brahmanage et al. (2020)
C. flammulae	MFLU 20-0397^{T}	MT370397	MT370422	MT370368	MT729651	Brahmanage et al. (2020)
C. flammulae	MFLU 20-0399	MT370395	MT370420	MT370366	—	Brahmanage et al. (2020)
C. galatellae	MFLUCC 18-0773^{T}	MN632549	MN632550	MN632551	—	Hongsanan et al. (2020)
C. incompta	CBS 467.76	—	GU238087	GU238220	KC584504	Aveskamp et al. (2010)
C. incompta	CH-16	KU973716	KU973729	—	—	Moral et al. (2017)
C. italica	MFLUCC 15-0073^{T}	KX500109	—	—	—	Tibpromma et al. (2015)
C. lini	MFLUCC 14-0968^{T}	KR049218	KR049219	KT210389	—	Wanasinghe et al. (2015)
C. lini	MFLUCC 14-0561	KT591614	KT591615	KT591616	—	Wanasinghe et al. (2015)

Taxon name	Strain number	ITS	LSU	SSU	*rpb2*	References
C. lonicerae	MFLU 20-0385^{T}	MT370394	MT370419	MT370365	MT729649	Brahmanage et al. (2020)
C. lonicerae	MFLU 18-1236	OL744429	OL744433	OL744435	OL771441	Brahmanage et al. (2020)
C. neimengguensis	GMBCC2306^{T}	PX314703	PX314701	PX314705	PX310456	Unpublished
C. neimengguensis	GMBCC2319	PX314704	PX314702	PX314706	PX310457	Unpublished
C. permunda	MFLUCC 14-0974	KY659561	KY659564	KY659568	–	Vu et al. (2019)
C. pimpinellae	MFLUCC 14-1159^{T}	KU987665	KU987666	KU987667	–	Li et al. (2016)
C. rosae	MFLU 15-0203^{T}	MG828876	MG828992	MG829103	MG829249	Wanasinghe et al. (2018)
C. rosae	MFLU 16-0234	MG828877	MG828993	MG829104	MG829250	Wanasinghe et al. (2018)
C. rosarum	MFLUCC 14-0962^{T}	MG828878	MG828994	MG829105	MG829251	Wanasinghe et al. (2018)
C. rosigena	MFLU 16-0229^{T}	MG828879	MG828995	MG829106	MG829252	Wanasinghe et al. (2018)
C. sedi	MFLUCC 13-0763^{T}	KP334717	KP334707	KP334727	–	Ariyawansa et al. (2014)
C. sedi	MFLUCC 13-0817	KP334715	KP334705	KP334725	–	Ariyawansa et al. (2014)
C. spartii	MFLUCC 13-0214^{T}	KM577159	KM577160	KM577161	–	Crous et al. (2014)
C. typhicola	CBS 602.72	MH860592	MH872288	–	–	Vu et al. (2019)
C. xanthoceratis	CCMJ 13078^{T}	OQ534245	OQ534241	OQ676456	OQ547802	Xu et al. (2024)
C. xanthoceratis	CCMJ 13079	OQ534246	OQ534242	OQ676457	OQ547803	Xu et al. (2024)
C. xiangshawanensis	**GMBCC2305^{T}**	**PX660510**	**PX660514**	**PX660506**	**PX672977**	**This study**
C. xiangshawanensis	**GMBCC2318**	**PX660511**	**PX660515**	**PX660507**	**PX672978**	**This study**
Neocamarosporium betae	CBS 523.66	FJ426981	MH870520	EU754080	KT389670	Aveskamp et al. (2009)
N. calvescens	CBS 246.79	MH861203	EU754131	EU754032	KC584500	Vu et al. (2019)

Results

Phylogenetic analyses

The phylogenetic trees obtained from RAxML and Bayesian Inference analyses were essentially similar. The RAxML analysis of the combined dataset yielded the best-scoring tree (Fig. 2), which consisted of 41 taxa, and the final alignment comprised 4029 characters, including gaps (ITS: 1–540, LSU: 541–1922, *rpb2*: 1923–3083, SSU: 3084–4029). The final ML optimization likelihood value was -14494.444982. The matrix contained 935 distinct alignment patterns, with 34.05% of characters undetermined or missing. Parameters for the GTR+I+G model of the combined ITS, LSU, *rpb2*, and SSU were as follows: estimated base frequencies A = 0.254158, C = 0.228977, G = 0.268187, T = 0.248678; substitution rates AC = 1.928002, AG = 4.366339, AT = 1.437220, CG = 1.029313, CT = 7.549462, GT = 1.0; proportion of invariable sites I = 0.641653; and gamma distribution shape parameter α = 0.725266. The final RAxML tree is shown in Fig. 2.

In our phylogenetic analyses, we obtained results consistent with those of recent publications by Mattoo et al. (2023) and Xu et al. (2024). Our new species, *Comoclathris desertica* (GMBCC2307 and GMBCC2320), was well separated from *C. clematidis* R. Xu, Phukhams. & Yu Li (CCMJ 13076 and CCMJ 13077) and *C. xanthoceratis* R. Xu, Phukhams. & Yu Li (CCMJ 13078 and CCMJ 13079) in a distinct lineage with 100% ML/1.00 PP statistical support; *Comoclathris xiangshawanensis* (GMBCC2305 and GMBCC2318) was well separated from *C. antarctica* Istel, J. Pawłowska & Wrzosek (WA0000074564, ex-type) with 87% ML/0.98 PP statistical support.

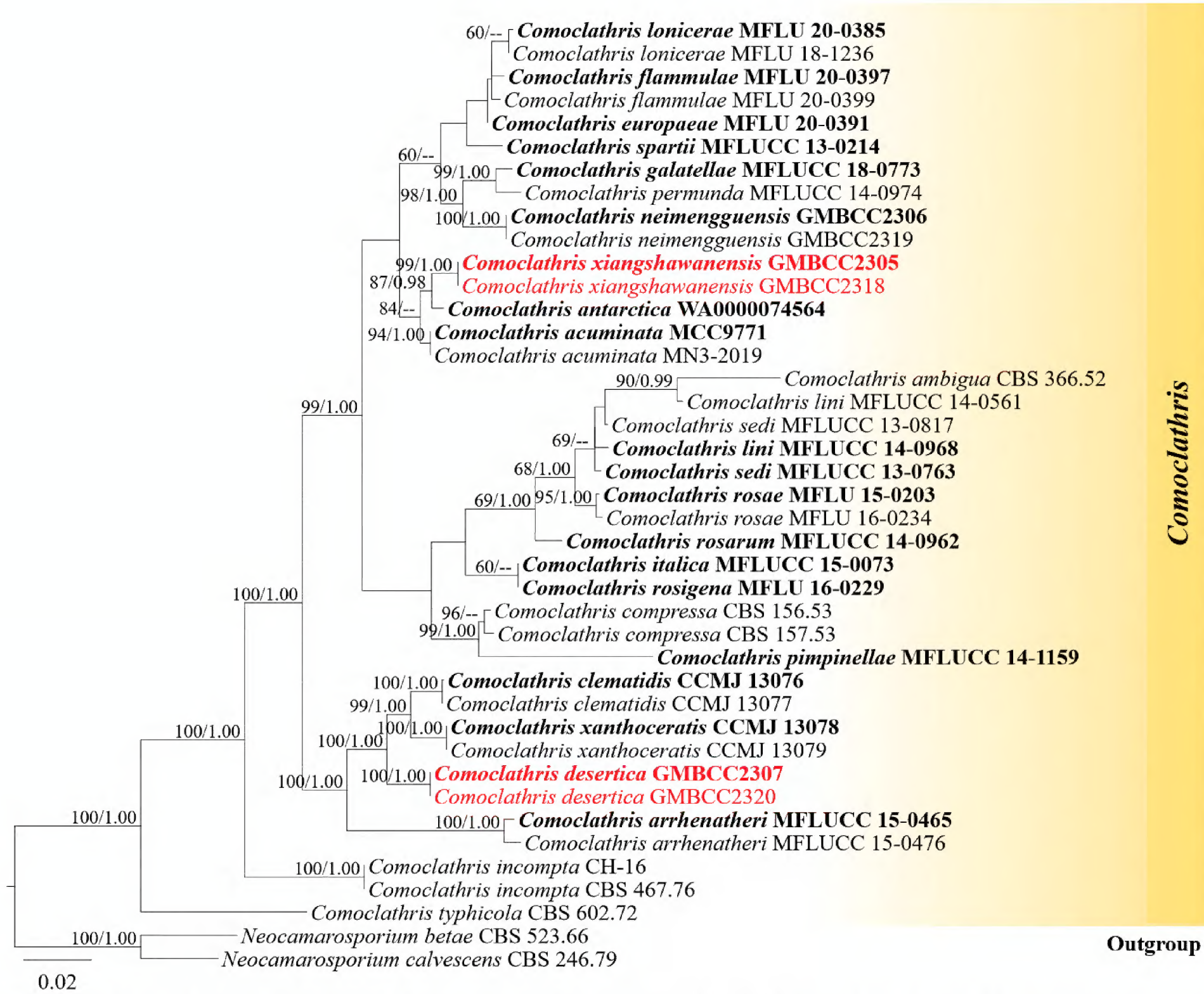

Figure 2. Maximum likelihood consensus tree inferred from the combined ITS, LSU, *rpb*2, and SSU multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 60% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given near the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Neocamarosporium betae* (CBS 523.66) and *N. calvescens* (CBS 246.79). The new isolates are indicated in red, and the ex-type strains are in bold.

Taxonomy

Comoclathris desertica **X.G. Tian, T.Y. Du & D.F. Bao, sp. nov.**

MycoBank No: MB861793

Facesoffungi Number: FoF19021

Fig. 3

Etymology. Named after the desert habitat from where the holotype was collected.

Holotype. GMB-W1518.

Description. ***Saprobic*** on dead branches of an unidentified wood. **Sexual morph**: ***Ascomata*** 90–200 × 70–190 µm ($\bar{x}$ = 115 × 116 µm, n = 5), solitary, scattered or aggregated, immersed, not obvious on the surface of the host, subglobose, black, ostiole not obvious. ***Peridium*** 10–30 µm wide, comprising

thin-walled cells of ***textura angularis***, dark brown to black. ***Hamathecium*** comprising numerous, 2 µm wide, filamentous, septate, branched, cellular pseudoparaphyses, hyaline, embedded in a gelatinous matrix, extending above the asci. ***Asci*** 65–85 × 18–23 µm ($\bar{x}$ = 76 × 20 µm, n = 30), bitunicate, fissitunicate, 8-spored, cylindrical-clavate, short pedicellate, apically rounded. ***Ascospores*** 16–23 × 8–10 µm ($\bar{x}$ = 19 × 9 µm, n = 30), 1-seriate, slightly overlapping, fusiform, initially yellowish, becoming brown to dark brown, muriform, with 3 transversely septa and 1 vertical septum, consisting of 6 cells, upper end conical, lower end tapered gradually, apical cell mostly undivided, straight or slightly curved, smooth-walled, surrounded by a mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics. Ascospores germinated on PDA within 12 h at 28 °C, and germ tubes were produced around spores. Colonies on PDA reached 2 cm diam. after one week at 28 °C. Colonies obverse: circular, white-cream to grey, with sparsely hairy edge; grey from below, the active hyphae at the edge are white.

Material examined. CHINA • Inner Mongolia Autonomous Region, Ordos City, Xiangshawan, on dead branches of an unidentified wood in the desert, 01 October 2023, J.Y. Zhang, BTD24 (GMB-W1518, holotype), ex-type, GMBCC2307, other living culture, GMBCC2320.

GenBank numbers. GMBCC2307: ITS = PX660512, LSU = PX660516, SSU = PX660508, *rpb2* = PX672979; GMBCC2320: ITS = PX660513, LSU = PX660517, SSU = PX660509, *rpb2* = PX672980.

Notes. *Comoclathris desertica* clustered with *C. clematidis* (CCMJ 13076, ex-type and CCMJ 13077) and *C. xanthoceratis* (CCMJ 13078, ex-type and CCMJ 13079) in the phylogenetic tree with 100% in ML and 1.00 in BYPP statistical support (Fig. 2). A nucleotide base pair differences between our new strain (GMBCC2307, ex-type) and *C. clematidis* (CCMJ 13076, ex-type) in ITS, LSU, SSU, and *rpb2* (without gaps) showed a 2.70% (14/519 bp) difference in ITS, 1.33% (9/679 bp) difference in LSU, 0.32% (2/628 bp) difference in SSU, and 5.58% (47/842 bp) difference in *rpb2*. Between our new strain (GMBCC2307, ex-type) and *C. xanthoceratis* (CCMJ 13078, ex-type), there was a 2.35% (12/510 bp) difference in ITS, 1.18% (8/676 bp) difference in LSU, 0.32% (2/628 bp) difference in SSU, and 6% (52/866 bp) difference in *rpb2*.

Morphologically, *C. desertica* is similar to *C. clematidis* and *C. xanthoceratis*, both of which have ascospores with 3 transverse septa and a vertical septum, surrounded by a thick mucilaginous sheath. But *C. desertica* is different from *C. clematidis* and *C. xanthoceratis* in having immersed ascomata, and dark brown ascospores, 1-seriate, slightly overlapping, smooth-walled; while *C. clematidis* has immersed to erumpent ascomata, and brown ascospores, with verrucose or echinulate wall (Xu et al. 2024); while *C. xanthoceratis* has immersed to semi-immersed ascomata, and brown to dark brown ascospores, 1–2-seriate (Xu et al. 2024). And our collection displays comparatively smaller ascospores than these two species (viz., *C. desertica*: 19 × 9 µm, *C. clematidis*: 30 × 14 µm, *C. xanthoceratis*: 37 × 16 µm).

Therefore, *C. desertica* is introduced as a new species from China based on morphological and molecular evidence as recommended by Jeewon and Hyde (2016).

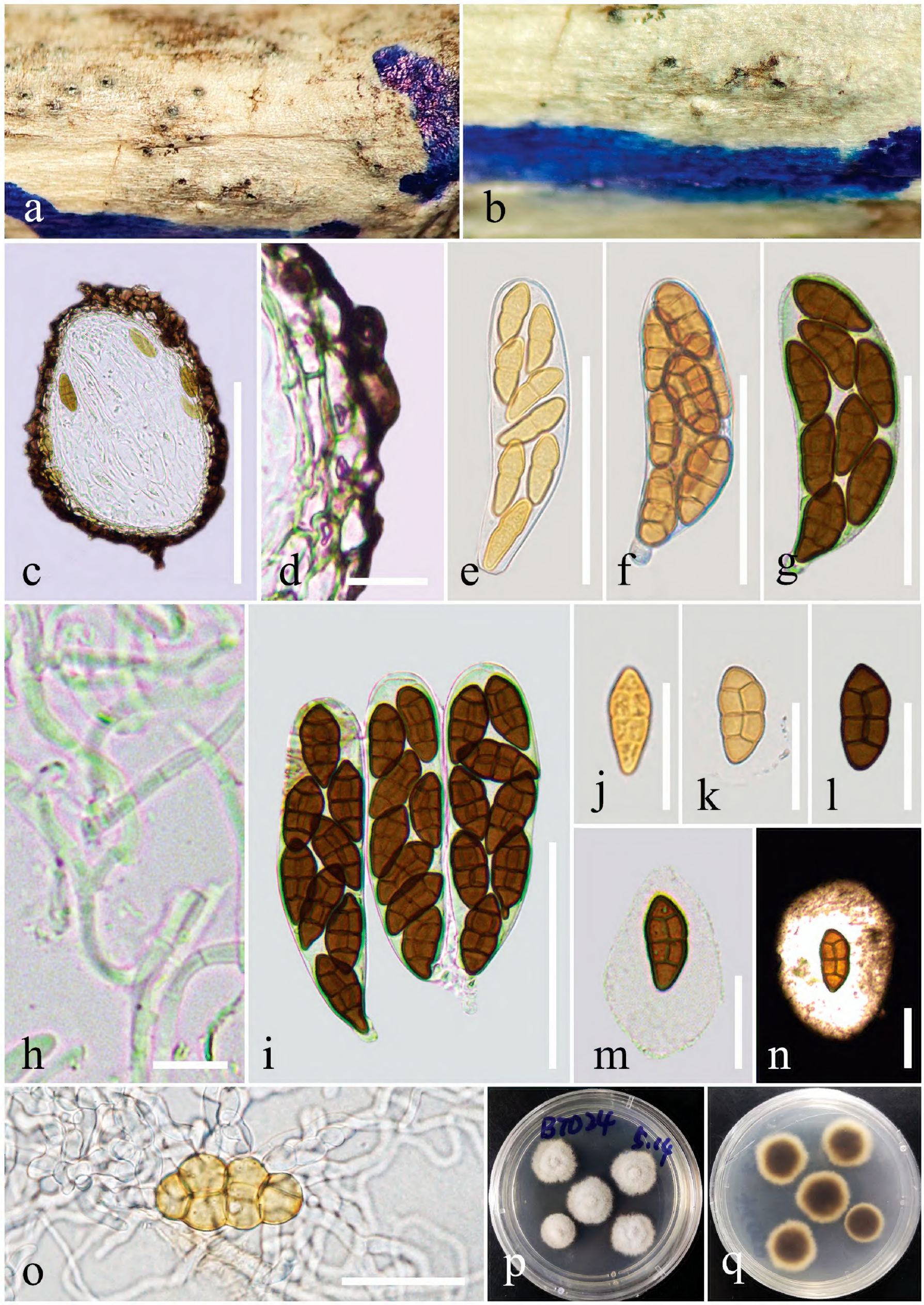

Figure 3. *Comoclathris desertica* (GMB-W1518, holotype). **a**, **b.** Appearance of ascomata on the substrate; **c.** Section through an ascoma; **d.** Peridium; **e-g, i.** Asci; **h.** Pseudoparaphyses; **j–n.** Ascospores (**m, n** surrounded by mucilaginous sheath); **o.** A germinated ascospore; **p, q.** Colonies on PDA from above and below after one week. Scale bars: 100 µm (**c**); 10 µm (**d, h**); 50 µm (**e-g, i**); 20 µm (**j–o**).

Comoclathris xiangshawanensis **X.G. Tian, T.Y. Du & D.F. Bao, sp. nov.**
MycoBank No: MB861794
Facesoffungi Number: FoF19022
Fig. 4

Etymology. Named after the type locality, "the desert region of Xiangshawan, China".

Holotype. GMB-W1526.

Description. ***Saprobic*** on dead branches of an unidentified wood. **Sexual morph**: ***Ascomata*** 100–200 × 90–200 µm ($\bar{x}$ = 132 × 118 µm, n = 10), solitary, scattered or aggregated into small groups, semi-immersed, subglobose, black, ostiole not obvious. ***Peridium*** 10–20 µm wide, comprising thin-walled cells of ***textura angularis***, dark brown to black. ***Hamathecium*** comprising numerous, 2 µm wide, filamentous, septate, branched, cellular pseudoparaphyses, hyaline, embedded in a gelatinous matrix, extending above the asci. ***Asci*** 65–85 × 15–23 µm ($\bar{x}$ = 73 × 21 µm, n = 30), bitunicate, fissitunicate, 8-spored, cylindrical-clavate, short pedicellate, apically rounded. ***Ascospores*** 17–23 × 7–11 µm ($\bar{x}$ = 19 × 8.5 µm, n = 30), 1–2-seriate, broadly fusiform, initially yellowish, becoming brown, muriform, with 5(–6) transversely septa and 1–2 vertical septa, consisting of 9–14 cells, with conical or obtuse ends, straight or slightly curved, smooth-walled, surrounded by a mucilaginous sheath. **Asexual morph**: Undetermined.

Culture characteristics. Ascospores germinated on PDA within 12 h at 28 °C and germ tubes were produced around spores. Colonies on PDA reached 2 cm diam. after one week at 28 °C. Colonies obverse: circular, white-cream, with sparsely hairy edge; cream to light yellow from below.

Material examined. CHINA • Inner Mongolia Autonomous Region, Ordos City, Xiangshawan, on dead branches of an unidentified wood in the desert, 01 October 2023, J.Y. Zhang, BTD16 (GMB-W1526, holotype), ex-type, GMBCC2305, other living culture, GMBCC2318.

GenBank numbers. GMBCC2305: ITS = PX660510, LSU = PX660514, SSU = PX660506, *rpb2* = PX672977; GMBCC2318: ITS = PX660511, LSU = PX660515, SSU = PX660507, *rpb2* = PX672978.

Notes. *Comoclathris xiangshawanensis* clustered with *C. antarctica* (WA0000074564, ex-type) and *C. acuminata* Mattoo, Nonzom & A. Ghosh (MCC9771, ex-type and MN3-2019) in the phylogenetic tree (Fig. 2). A comparison of nucleotide base pair differences between our new strain (GMBCC2305, ex-type) and *C. antarctica* (WA0000074564, ex-type) in ITS and LSU, the result (without gaps) showed a 1.65% (8/484 bp) difference in ITS, 0.24% (2/818 bp) difference in LSU. Between our new strain (GMBCC2305, ex-type) and *C. acuminata* (MCC9771, ex-type) in ITS and LSU, the result (without gaps) showed a 1.86% (9/484 bp) difference in ITS, 0.25% (2/807 bp) difference in LSU (*C. antarctica* (WA0000074564, ex-type) and *C. acuminata* (MCC9771, ex-type) have no available SSU and *rpb2* sequences in NCBI and hence cannot be compared).

Morphologically, *C. xiangshawanensis* differs from *C. antarctica* and *C. acuminata* in having brown ascospores with 5(–6) transversely septa and 1–2 vertical septa, consisting of 9–14 cells, surrounded by a mucilaginous sheath; while *C. antarctica* has ascospores with 6–8 transvers septa, consisting of 10–17 cells (Crous et al. 2021); while *C. acuminata* has dark brown ascospores, with 3–8 transverse septa, 3–5 vertical septa, consisting of 15–21

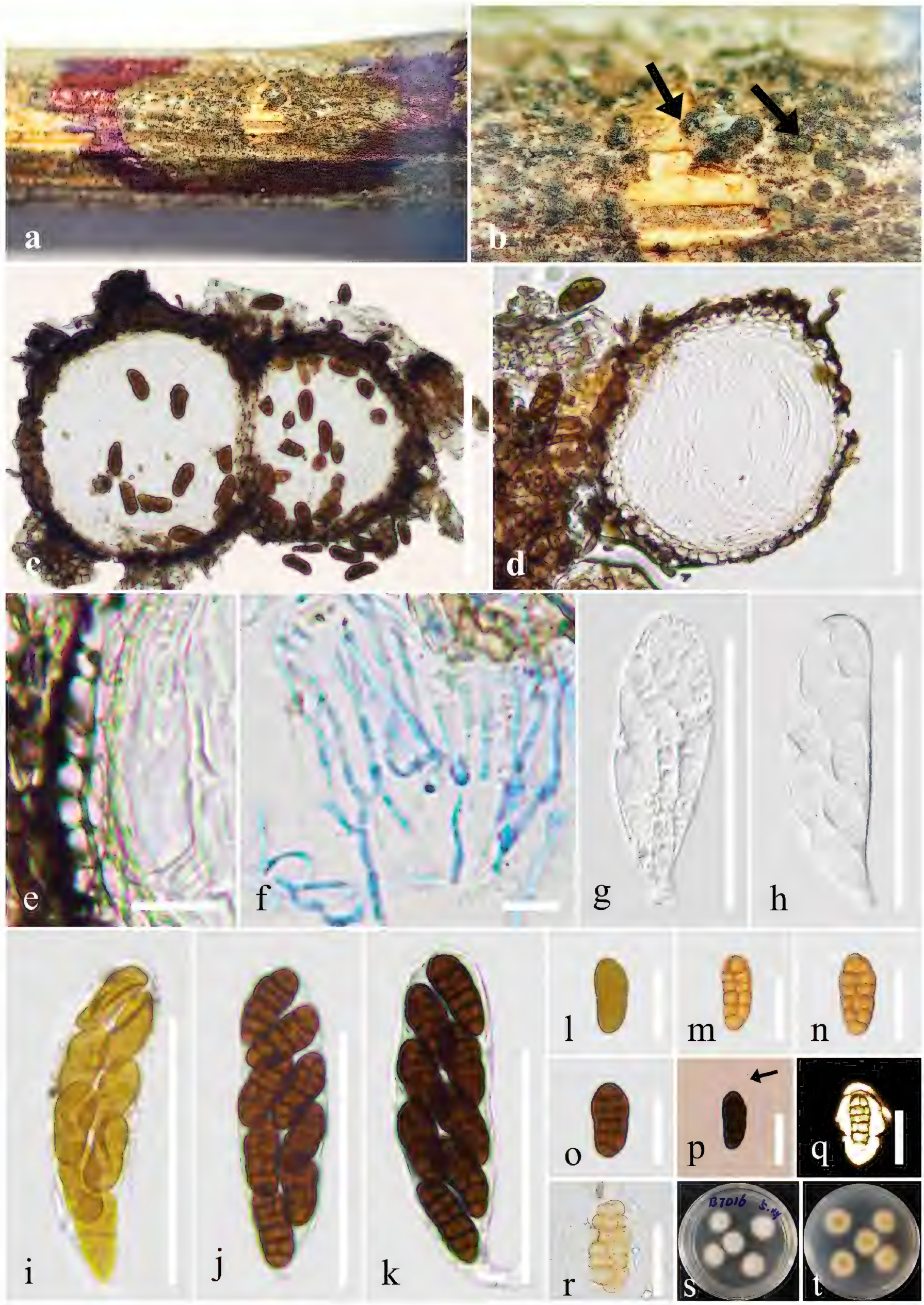

Figure 4. *Comoclathris xiangshawanensis* (GMB-W1526, holotype). **a, b.** Appearance of ascomata on the substrate (arrows indicate black ascomata); **c, d.** Section through ascomata; **e.** Peridium; **f.** Pseudoparaphyses; **g–k.** Asci; **l–q.** Ascospores (arrow indicates mucilaginous sheath); **r.** A germinated ascospore; **s, t.** Colonies on PDA from above and below after one week. Scale bars: 100 μm (**c, d**); 10 μm (**e, f**); 50 μm (**g–k**); 20 μm (**l–r**).

cells, with a beak-like extension (Mattoo et al. 2023). In addition, our collection is saprobic on dead branches in desert areas in China, while *C. antarctica* is isolated from soil sample in Antarctica, and *C. acuminata* was isolated as an endophyte from the stem of *Ephedra gerardiana* Wall. in India (Mattoo et al. 2023).

Therefore, *C. xiangshawanensis* is introduced as a new species from China based on morphological and molecular evidence. To provide a better overview of the different morphologies associated with different *Comoclathris* species, we also compiled ascospore morphology and other ecological data in a table (Table 2).

Table 2. Morphological characteristics of ascospore and other ecological data of *Comoclathris* species. NA: Information not available.

Species	Ascospore			Hosts	Collection locations	References
	Color	Septa	Sheath			
Comoclathris acuminata	Dark brown	3–8 transverse septa and 3–5 vertical septa	N/A	*Ephedra gerardiana*	India	Mattoo et al. (2023)
Comoclathris antarctica	Yellow to pale brown	6–8 transverse septa	N/A	Soil sample	Antarctica	Crous et al. (2021)
Comoclathris arctica	Mid to dark reddish-brown	6 transverse septa and 1 vertical septum	With a sheath 2–3 µm wide	*Festucae brachyphyllae*, *Puccinellia angustata*	Canada	Shoemaker and Babcock (1992)
Comoclathris arrhenatheri	Yellow to pale brown	4 transverse septa and 2–3 vertical septa	Surrounded by a thick mucilaginous sheath	*Arrhenatherum elatius*	Italy	Thambugala et al. (2017)
Comoclathris bougainvilleae	N/A	N/A	N/A	*Bougainvillea spectabilis*	India	Patil and Ramesh (1987)
Comoclathris cichoriacearum	N/A	N/A	N/A	*Hieracium villosum*	N/A	Nograsek (1990)
Comoclathris clematidis	Brown	3 transverse septa and 1 vertical septum	Surrounded by a thick mucilaginous sheath	*Clematis* sp.	China	Xu et al. (2024)
Comoclathris compressa	Dark reddish-brown	3 transverse septa and 1 vertical septum	With a uniform sheath 2–3 µm wide	*Agastache urticifolia*, *Agoseris glauca*, *Aquilegia leptocera*, *Arternisia pedatzjidi*, *Balsatnorrhiza deltoidea*, *Brickellia grandijlora*, *Coleosanthus grandijlorus*, *Castilleja miniata*, *Clematis hirsutissirna*, *Helianthella* sp., *Helianthus* sp., *Juncus balticus*, *Ligusticum purpureum*, *Lupinus parvijlorus*, *Penstemon* sp., *Polygonum alpina*, *Rudbeckia* sp., *Senecio thapsoides*, *Valeriana* sp., *Viguiera multijlora*, *Wyethia mollis*, *Wyethia* sp., *Xerophyllum tenux*	USA	Shoemaker and Babcock (1992)
Comoclathris depressa	Mid yellowish-brown	3 transverse septa and 1 vertical septum	With a sheath 2–3 µm wide	*Arabis* sp., *Lotnatiutn dissectum*	USA	Shoemaker and Babcock (1992)
Comoclathris emodi	Dark yellowish-brown	4 transverse septa and 1 vertical septum	With a sheath 1.5–4 µm wide	*Festucae lucidae*	India	Shoemaker and Babcock (1992)
Comoclathris europaeae	Brown	7 transverse septa and 1 vertical septum	Surrounded by amucilaginous sheath	*Olea europaea*	Italy	Brahmanage et al. (2020)

Species	Ascospore			Hosts	Collection locations	References
	Color	Septa	Sheath			
Comoclathris extrema	Dark reddish-brown	4 transverse septa and 1 vertical septum	With a sheath 2–3 µm wide	*Lini perenni*	India	Shoemaker and Babcock (1992)
Comoclathris flammulae	Dark brown	6 transverse septa and 1–2 vertical septa	Mucilaginous sheath	*Clematis flammula*, *Colutea arborescens*	Italy	Brahmanage et al. (2020)
Comoclathris galatellae	Brown or pale brown	2–4 transverse septa and 1–2 vertical septa	Without sheath	*Galatella villosa*	Russia, Ukraine	Hongsanan et al. (2020)
Comoclathris harperi	Mid reddish-brown	7 transverse septa and 1 vertical septum	With a sheath 1–2 µm wide	*Carex rupestris*, *Hierochloe alpina*	Sweden	Shoemaker and Babcock (1992)
Comoclathris incompta	N/A	N/A	N/A	*Olea europaea*	Greece, Italy	Ariyawansa et al. (2015)
Comoclathris indica	N/A	N/A	N/A	*Arachis hypogaea*	India	Patil and Pawar (1987)
Comoclathris italica	Brown	6–8 transverse septa and 1–2 vertical septa	Mucilaginous sheath	*Dactylis glomerata*	Italy	Thambugala et al. (2017)
Comoclathris lanata	Brown to reddish-brown	4–5 transverse septa and 1–2 vertical septa	Surrounded by a distinct, hyaline, mucilaginous 3–8 µm wide sheath	*Leptotaenia multifida*	USA	Ariyawansa et al. (2015)
Comoclathris lini	yellowish-brown	3–5 transverse septa and 1–2 vertical septa	With a thick mucilaginous sheath	*Linum* sp.	Italy	Wanasinghe et al. (2015)
Comoclathris lonicerae	yellowish-brown	3–5 transverse septa and 1–2 vertical septa	With a thick mucilaginous sheath	*Lonicera* sp.	Italy	Brahmanage et al. (2020)
Comoclathris magna	Dark reddish-brown	3 transverse septa and 1 vertical septum	With a sheath 2–4 µm wide	*Anemone occidentalis*, *Chlorogalum pomeridianum*, *Helianthella californica*, *Linum perenne*, *Lomatium nudicaule*, *Penstemon gracilentus*, *Sphenosciadium capitellatum*, umbellifer	USA	Shoemaker and Babcock (1992)
Comoclathris miliarakisii	N/A	N/A	N/A	*Sclerochorton junceum*	Greece	Petrak (1938)
Comoclathris persica	Mid reddish-brown	4 transverse septa and 1 vertical septum	With a uniform sheath 3–4 µm wide	*Dianthus orientalis*	Iran	Shoemaker and Babcock (1992)
Comoclathris pimpinellae	Yellow to light brown	3 transverse septa and 2 vertical septa	Surrounded by a thick, hyaline, a mucilaginous sheath	*Pimpinella tragium*	Russia	Li et al. (2016)
Comoclathris platysporioides	Dark reddish-brown	5 transverse septa and 1 vertical septum	With a uniform sheath, 1–2 µm wide	*Selaginella wrightii*	USA	Shoemaker and Babcock (1992)
Comoclathris pseudoverruculosa	N/A	N/A	N/A	*Carex firma*	N/A	Nograsek (1990)
Comoclathris pyrenophoroides	N/A	N/A	N/A	*Festuca* and *Bromus*	Italy	Checa (1998)
Comoclathris quadriseptata	Mid reddish-brown	4 transverse septa and 1 vertical septum	With a uniform sheath 1–2 µm wide	*Agropyron divergens*, *Avena pratensis*, *Dianthus orientalis*, *Matthiola* sp., *Poaceae*, *Sporobolus cryptandrus*	Canada	Shoemaker and Babcock (1992)
Comoclathris rosae	Pale brown	4–7 transverse septa and 1–2 vertical septa	Surrounded by a thick mucilaginous sheath	*Rosa canina*	Italy	Wanasinghe et al. (2018)

Species	Ascospore			Hosts	Collection locations	References
	Color	Septa	Sheath			
Comoclathris rosarum	Brown	6–7 transverse septa and 2–4 vertical septa	Surrounded by a thick mucilaginous sheath	*Rosa canina*	Italy	Wanasinghe et al. (2018)
Comoclathris rosigena	Pale brown	5–7 transverse septa and 1 vertical septum	Surrounded by a thick mucilaginous sheath	*Rosa canina*	Italy	Wanasinghe et al. (2018)
Comoclathris salsolae	Mid yellowish-brown	4 transverse septa and 1 vertical septum	With a uniform sheath 2–3 µm wide	*Ipomoea leptoplzylla*, *Salsola* sp.	USA	Shoemaker and Babcock (1992)
Comoclathris sedi	Brown to reddish-brown	4–5 transverse septa and 1–2 vertical septa	Surrounded by a distinct, hyaline, mucilaginous 5–9 µm wide sheath	*Clematis vitalba*, *Rosa* sp., *Sedum* sp.	Italy	Ariyawansa et al. (2015)
Comoclathris sisyrinchii	Mid yellowish-brown	3 transverse septa and 1 vertical septum	N/A	*Carpha alina*, *Lomatium californicuin*, *Sisyrinchium junceum*, *Sisyrinchium middletoni*	USA	Shoemaker and Babcock (1992)
Comoclathris sororia	Dark reddish-brown	3 transverse septa and 1 vertical septum	N/A	*Dianthus orientalis*	Turkey	Shoemaker and Babcock (1992)
Comoclathris spartii	Yellow to pale brown	Muriform	Surrounded by a mucilaginous sheath	*Spartium junceum*	Italy	Crous et al. (2014)
Comoclathris subdeflectens	N/A	N/A	N/A	*Ranunculus montanus*	N/A	Nograsek (1990)
Comoclathris typhicola	Brown	3 transverse septa and 1 vertical septum	N/A	*Typha latifolia*, *Typha angustifolia*	Austria, Denmark, England, Germany, India, Iran, Netherlands, Pakistan, Poland, Portugal, Russia, Switzerland, and USA	Cooke (1872); Webster and Lucas (1959); Shoemaker and Babcock (1992); Boerema et al. (2004); Ahmadpour et al. (2024)
Comoclathris utahensis	Dark reddish-brown	3 transverse septa and 1 vertical septum	With a sheath 1–3 µm wide	*Arternisia scopulorurn*, *Brickelliaun bellata*, *Castilleja rniniata*, *Eupatoriurn occidentale*, *Linurn perenne*, *Linum perenne* L., *Polygonurn arnphibiurn*, *Senecio* sp., *Silene lnontana*	USA	Shoemaker and Babcock (1992)
Comoclathris verrucosa	Dark reddish-brown	3 transverse septa and 1 vertical septum	With a uniform sheath 2–3 µm wide	*Juncus balticus*	USA	Shoemaker and Babcock (1992)
Comoclathris verruculosa	Mid reddish-brown	5 transverse septa and 1 vertical septum	With a uniform sheath 1.5–3.5 µm wide	*Deschampsia caespitosa*, *Poa glauca*	Finland, Norway, Switzerland	Shoemaker and Babcock (1992)
Comoclathris wehmeyeri	N/A	N/A	N/A	*Crossandra infundibuliformis*	India	Pande (1980)
Comoclathris xanthoceratis	Brown to dark brown	3 transverse septa and 1 vertical septum	Surrounded by a thick mucilaginous sheath	*Xanthoceras sorbifolium*	China	Xu et al. (2024)
Comoclathris xerophila	Mid reddish-brown	3 transverse septa and 1 vertical septum	N/A	*Scleropogon brevifolius*	Argentina	Shoemaker and Babcock (1992)

Discussion

Comoclathris is a widely distributed genus, recorded on all five continents viz. Asia, Europe, Africa, the Americas, and Antarctica (Mattoo et al. 2023; Xu et al. 2024). Recent studies in China and other regions have shown that *Comoclathris* species are distributed in a variety of environments and substrates, from humid forests to semi-arid deserts (Mattoo et al. 2023; Xu et al. 2024; this study), suggesting that their diversity and ecological adaptability may be underestimated. The discovery of *C. desertica* and *C. xiangshawanensis* in desert wood in Inner Mongolia further expands the known distribution of this genus, providing valuable data for the global taxonomic system of *Comoclathris*. Furthermore, the thick, gelatinous sheaths enclosing the ascospores of these two species highlight the adaptability to extremely arid environments of these species. This is in line with the general characteristics of this genus, with obvious mucilaginous sheaths surrounding the ascospores. Based on morphological information currently available for this genus (Table 2), most species have mucilaginous sheaths, with only seven species having no record of mucilaginous sheaths (viz., *C. acuminata*, *C. antarctica*, *C. galatellae* D. Pem, Bulgakov & K.D. Hyde, *C. sisyrinchii* (Speg.) Shoemaker & C.E. Babc., *C. sororia* (Bubák) Shoemaker & C.E. Babc., *C. typhicola* (Cooke) H.A. Ariy. & K.D. Hyde, and *C. xerophila* (Speg.) Shoemaker & C.E. Babc.) (Cooke 1872; Shoemaker and Babcock 1992; Hongsanan et al. 2020; Crous et al. 2021; Mattoo et al. 2023).

Although 52 epithets are listed in Index Fungorum (2026), only 21 species have molecular data in NCBI, and the naming of many historical species is based solely on morphological characteristics. The lack of DNA sequences, type specimen revisions, and living cultures hinder phylogenetic analysis and species delineation. Therefore, future work should collect more specimens and supplement them with molecular data of extant species to clarify species boundaries and evolutionary relationships.

Inner Mongolia is a typical semi-arid region where long-term grazing and desertification have led to the degradation of grasslands and soils. Fungi play a crucial role in the decomposition of organic matter and nutrient cycling in fragile ecosystems, but the diversity of saprobic fungi remains poorly understood. The discovery of two new *Comoclathris* species in the Xiangshawan desert demonstrates that even degraded or arid habitats can foster rich and unique fungal communities. These fungal groups reflect the potential ecological resilience and adaptive evolution of microfungi under extreme temperature and humidity fluctuations. This study not only enriches the known fungal diversity in northern China but also highlights the importance of ongoing mycological surveys in arid grassland and desert ecosystems for taxonomic progress and ecological conservation.

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Additional information

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Conceptualization: XGT. Data curation: ADM, TYD. Formal analysis: XGT, RJ. Funding acquisition: DFB. Investigation: TYD. Methodology: XGT, TYD. Project administration: DFB, XGT. Resources: TYD. Software: ADM, TYD. Supervision: RJ, SCK, ST. Validation: RJ, DFB. Visualization: TYD, XGT. Writing – original draft: XGT. Writing – review and editing: RJ, ST, SCK.

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Data availability

All of the data that support the findings of this study are available in the main text.

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